

This page gives you Search Results detail for the Application 10660968 and Search Result us-10-660-968a-38.rag.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:47:11 ; Search time 194 Seconds  
(without alignments)  
407.724 Million cell updates/sec

Title: US-10-660-968A-38  
Perfect score: 980  
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....QRRNLSSPCHPARRPVLSPK 173

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	980	100.0	173	4 AAU03118	Aau03118 Composite
2	980	100.0	173	6 ABP97852	Abp97852 Amino aci
3	969	98.9	175	6 ABP97851	Abp97851 Amino aci
4	969	98.9	197	3 AAB01421	Aab01421 Human TAN
5	815	83.2	267	4 AAU03114	Aau03114 Human ute
6	813	83.0	198	6 ABP97850	Abp97850 Amino aci

7	813	83.0	206	3	AAB01420	Aab01420	Human	TAN
8	813	83.0	231	3	AAy77468	Aay77468	Human	Ran
9	813	83.0	231	6	ABP97849	Abp97849	Amino	aci
10	813	83.0	231	6	AAO26531	Aao26531	231	resid
11	813	83.0	269	4	AAU03106	Aau03106	Human	ute
12	813	83.0	269	6	ABP97848	Abp97848	Amino	aci
13	813	83.0	269	6	ABU62739	Abu62739	Human	tum
14	813	83.0	297	4	AAU03113	Aau03113	Human	ute
15	813	83.0	299	4	AAU03116	Aau03116	Composite	
16	812	82.9	267	6	ABP97853	Abp97853	Amino	aci
17	810	82.7	297	4	AAB29534	Aab29534	Human	TNF
18	810	82.7	297	6	ABP97846	Abp97846	Amino	aci
19	810	82.7	297	6	ABU62740	Abu62740	Human	tum
20	810	82.7	297	7	AAE39991	Aae39991	Human	DNA
21	810	82.7	297	9	ADZ67769	Adz67769	Human	tum
22	810	82.7	299	3	AAB33477	Aab33477	Human	PRO
23	810	82.7	299	3	AAB30547	Aab30547	Amino	aci
24	810	82.7	299	4	AAB29533	Aab29533	Human	TNF
25	810	82.7	299	6	ABP97847	Abp97847	Amino	aci
26	810	82.7	299	7	AAE39990	Aae39990	Human	DNA
27	810	82.7	299	8	ADH54640	Adh54640	Human	DNA
28	759	77.4	231	4	AAB35335	Aab35335	Human	TR1
29	759	77.4	231	5	AAE26263	Aae26263	Human	TR1
30	759	77.4	231	6	ABO53260	Abo53260	Human	tum
31	759	77.4	231	7	ABR61979	Abr61979	Human	DEX
32	759	77.4	231	9	AED66552	Aed66552	Human	25
33	447.5	45.7	423	2	AAW93581	Aaw93581	Human	hAP
34	447.5	45.7	423	3	AAB23547	Aab23547	Human	Tro
35	447.5	45.7	423	6	ABR42031	Abr42031	Human	omo
36	447.5	45.7	423	6	ABU62750	Abu62750	Human	tum
37	447.5	45.7	423	10	AEF39142	Aef39142	Human	TAJ
38	447.5	45.7	423	10	AEF82598	Aef82598	Human	TAJ
39	444.5	45.4	210	2	AAy22223	Aay22223	Human	TNF
40	444.5	45.4	210	3	AAB28555	Aab28555	Human	TNF
41	443.5	45.3	328	2	AAy06400	Aay06400	Human	NTR
42	443.5	45.3	328	6	ABR42033	Abr42033	Human	omo
43	443.5	45.3	417	2	AAW70386	Aaw70386	Amino	aci
44	443.5	45.3	417	2	AAW98146	Aaw98146	Human	TRA
45	443.5	45.3	417	3	AAB33474	Aab33474	Human	PRO

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:56:11 ; Search time 51 Seconds  
(without alignments)  
296.918 Million cell updates/sec

Title: US-10-660-968A-38  
Perfect score: 980  
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....QRRNLSSPCHPARRPVLSKP 173

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	810	82.7	297	2	US-09-548-130-6 Sequence 6, Appli
2	810	82.7	297	2	US-09-949-016-7016 Sequence 7016, Ap
3	810	82.7	297	2	US-09-949-016-11181 Sequence 11181, A
4	810	82.7	299	2	US-09-548-130-3 Sequence 3, Appli
5	810	82.7	299	2	US-10-119-466-12 Sequence 12, Appl
6	759	77.4	231	2	US-10-046-433-61 Sequence 61, Appl
7	447.5	45.7	423	2	US-09-490-187-2 Sequence 2, Appli
8	444.5	45.4	210	2	US-09-286-529-3 Sequence 3, Appli
9	427	43.6	159	2	US-10-046-433-7 Sequence 7, Appli

10	427	43.6	226	2	US-10-046-433-5	Sequence 5, Appli
11	395.5	40.4	151	2	US-09-286-529-4	Sequence 4, Appli
12	167	17.0	448	2	US-09-342-681C-17	Sequence 17, Appl
13	167	17.0	448	2	US-09-342-681C-19	Sequence 19, Appl
14	150.5	15.4	186	1	US-08-089-458B-6	Sequence 6, Appli
15	142.5	14.5	415	2	US-09-006-353A-6	Sequence 6, Appli
16	142.5	14.5	415	2	US-09-573-986-6	Sequence 6, Appli
17	142	14.5	419	2	US-08-509-024-7	Sequence 7, Appli
18	142	14.5	419	2	US-09-333-279-7	Sequence 7, Appli
19	142	14.5	419	2	US-09-631-780-7	Sequence 7, Appli
20	141	14.4	239	2	US-09-934-289A-44	Sequence 44, Appl
21	141	14.4	258	2	US-09-579-845-8	Sequence 8, Appli
22	141	14.4	277	2	US-09-934-289A-42	Sequence 42, Appl
23	139.5	14.2	283	2	US-08-509-024-2	Sequence 2, Appli
24	139.5	14.2	283	2	US-09-333-279-2	Sequence 2, Appli
25	139.5	14.2	283	2	US-09-072-993C-2	Sequence 2, Appli
26	139.5	14.2	283	2	US-09-631-780-2	Sequence 2, Appli
27	139.5	14.2	283	2	US-09-934-289A-13	Sequence 13, Appl
28	139.5	14.2	284	2	US-09-949-016-7971	Sequence 7971, Ap
29	138.5	14.1	283	5	PCT-US96-12374-2	Sequence 2, Appli
30	137.5	14.0	350	2	US-10-046-433-41	Sequence 41, Appl
31	136	13.9	260	2	US-09-006-353A-8	Sequence 8, Appli
32	136	13.9	260	2	US-09-573-986-8	Sequence 8, Appli
33	136	13.9	260	2	US-09-949-016-6047	Sequence 6047, Ap
34	136	13.9	293	2	US-09-949-016-7945	Sequence 7945, Ap
35	133	13.6	355	1	US-08-292-549-6	Sequence 6, Appli
36	133	13.6	355	2	US-09-006-353A-14	Sequence 14, Appl
37	133	13.6	355	2	US-09-573-986-14	Sequence 14, Appl
38	132	13.5	163	2	US-08-828-683A-13	Sequence 13, Appl
39	132	13.5	163	2	US-09-523-323-54	Sequence 54, Appl
40	132	13.5	227	2	US-08-974-022-48	Sequence 48, Appl
41	132	13.5	227	2	US-08-795-445A-48	Sequence 48, Appl
42	132	13.5	227	2	US-08-795-447A-48	Sequence 48, Appl
43	132	13.5	227	2	US-08-974-186-48	Sequence 48, Appl
44	132	13.5	227	2	US-08-795-446B-48	Sequence 48, Appl
45	132	13.5	227	2	US-08-706-945D-134	Sequence 134, App

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OM protein - protein search, using sw model

Run on: July 31, 2006, 20:08:06 ; Search time 177 Seconds  
(without alignments)  
452.747 Million cell updates/sec

Title: US-10-660-968A-38  
Perfect score: 980  
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....QRRNLSSPCHPARRPVLSPK 173

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	980	100.0	173	4	US-10-660-968-38	Sequence 38, Appl
2	969	98.9	197	3	US-09-796-753-10	Sequence 10, Appl
3	815	83.2	267	4	US-10-660-968-29	Sequence 29, Appl
4	813	83.0	206	3	US-09-796-753-8	Sequence 8, Appli
5	813	83.0	231	3	US-09-840-795-19	Sequence 19, Appl
6	813	83.0	268	4	US-10-231-426-1	Sequence 1, Appli
7	813	83.0	268	4	US-10-231-416-1	Sequence 1, Appli
8	813	83.0	269	4	US-10-660-968-2	Sequence 2, Appli
9	813	83.0	297	4	US-10-660-968-27	Sequence 27, Appl
10	813	83.0	299	4	US-10-660-968-35	Sequence 35, Appl

11	810	82.7	297	4	US-10-243-157-6	Sequence 6, Appli
12	810	82.7	297	5	US-10-967-527A-17	Sequence 17, Appl
13	810	82.7	299	4	US-10-119-466-12	Sequence 12, Appl
14	810	82.7	299	4	US-10-243-157-3	Sequence 3, Appli
15	810	82.7	299	4	US-10-413-053-12	Sequence 12, Appl
16	759	77.4	231	4	US-10-046-433-61	Sequence 61, Appl
17	759	77.4	231	6	US-11-132-285-61	Sequence 61, Appl
18	447.5	45.7	423	6	US-11-195-851-2	Sequence 2, Appli
19	444.5	45.4	210	3	US-09-877-156-3	Sequence 3, Appli
20	443.5	45.3	417	3	US-09-780-532-2	Sequence 2, Appli
21	443.5	45.3	417	4	US-10-052-586-474	Sequence 474, App
22	443.5	45.3	417	4	US-10-174-590-474	Sequence 474, App
23	443.5	45.3	417	4	US-10-176-758-474	Sequence 474, App
24	443.5	45.3	417	4	US-10-175-737-474	Sequence 474, App
25	443.5	45.3	417	4	US-10-174-581-474	Sequence 474, App
26	443.5	45.3	417	4	US-10-176-483-474	Sequence 474, App
27	443.5	45.3	417	4	US-10-176-749-474	Sequence 474, App
28	443.5	45.3	417	4	US-10-176-914-474	Sequence 474, App
29	443.5	45.3	417	4	US-10-176-915-474	Sequence 474, App
30	443.5	45.3	417	4	US-10-173-706-474	Sequence 474, App
31	443.5	45.3	417	4	US-10-175-738-474	Sequence 474, App
32	443.5	45.3	417	4	US-10-175-752-474	Sequence 474, App
33	443.5	45.3	417	4	US-10-176-482-474	Sequence 474, App
34	443.5	45.3	417	4	US-10-176-757-474	Sequence 474, App
35	443.5	45.3	417	4	US-10-176-913-474	Sequence 474, App
36	443.5	45.3	417	4	US-10-180-552-474	Sequence 474, App
37	443.5	45.3	417	4	US-10-180-557-474	Sequence 474, App
38	443.5	45.3	417	4	US-10-173-700-474	Sequence 474, App
39	443.5	45.3	417	4	US-10-174-572-474	Sequence 474, App
40	443.5	45.3	417	4	US-10-174-579-474	Sequence 474, App
41	443.5	45.3	417	4	US-10-174-582-474	Sequence 474, App
42	443.5	45.3	417	4	US-10-174-588-474	Sequence 474, App
43	443.5	45.3	417	4	US-10-175-739-474	Sequence 474, App
44	443.5	45.3	417	4	US-10-175-740-474	Sequence 474, App
45	443.5	45.3	417	4	US-10-175-743-474	Sequence 474, App

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OM protein - protein search, using sw model

Run on: July 31, 2006, 20:08:41 ; Search time 31 Seconds  
(without alignments)  
368.569 Million cell updates/sec

Title: US-10-660-968A-38  
Perfect score: 980  
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....QRRNLSSPCHPARRPVLSPK 173

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	443.5	45.3	417	6	US-10-196-749-474 Sequence 474, App
2	140.5	14.3	408	7	US-11-175-714-140 Sequence 140, App
3	140.5	14.3	430	6	US-10-539-228-522 Sequence 522, App
4	140.5	14.3	430	7	US-11-175-714-138 Sequence 138, App
5	139.5	14.2	283	6	US-10-539-228-546 Sequence 546, App
6	139.5	14.2	283	6	US-10-539-228-548 Sequence 548, App
7	139.5	14.2	283	6	US-10-539-228-550 Sequence 550, App
8	136	13.9	260	6	US-10-511-937-2519 Sequence 2519, Ap

9	132	13.5	355	6	US-10-504-973-33	Sequence 33, Appl
10	132	13.5	461	6	US-10-511-937-2945	Sequence 2945, Ap
11	132	13.5	461	7	US-11-183-218-32	Sequence 32, Appl
12	122	12.4	258	6	US-10-643-589-4	Sequence 4, Appli
13	121	12.3	255	6	US-10-623-808-8	Sequence 8, Appli
14	121	12.3	255	6	US-10-539-257-2	Sequence 2, Appli
15	121	12.3	255	7	US-11-128-422-8	Sequence 8, Appli
16	120.5	12.3	197	6	US-10-533-153-1	Sequence 1, Appli
17	117.5	12.0	256	6	US-10-623-808-6	Sequence 6, Appli
18	117.5	12.0	256	7	US-11-128-422-6	Sequence 6, Appli
19	112	11.4	247	6	US-10-504-973-6	Sequence 6, Appli
20	108	11.0	269	7	US-11-170-797-19	Sequence 19, Appl
21	106.5	10.9	194	6	US-10-539-228-543	Sequence 543, App
22	106.5	10.9	278	7	US-11-170-797-16	Sequence 16, Appl
23	106.5	10.9	1533	7	US-11-174-307B-78	Sequence 78, Appl
24	105.5	10.8	237	6	US-10-504-973-22	Sequence 22, Appl
25	102.5	10.5	417	6	US-10-505-928-793	Sequence 793, App
26	102	10.4	243	7	US-11-320-192-9	Sequence 9, Appli
27	101.5	10.4	349	7	US-11-175-714-67	Sequence 67, Appl
28	101.5	10.4	401	7	US-11-175-714-54	Sequence 54, Appl
29	101.5	10.4	1006	6	US-10-511-937-2425	Sequence 2425, Ap
30	101.5	10.4	1006	7	US-11-259-133-32	Sequence 32, Appl
31	101	10.3	243	7	US-11-320-192-12	Sequence 12, Appl
32	100.5	10.3	250	7	US-11-320-192-11	Sequence 11, Appl
33	100.5	10.3	1017	7	US-11-174-307B-956	Sequence 956, App
34	100	10.2	293	7	US-11-318-156-2	Sequence 2, Appli
35	98.5	10.1	251	7	US-11-320-192-8	Sequence 8, Appli
36	98.5	10.1	1744	7	US-11-174-307B-2750	Sequence 2750, Ap
37	98	10.0	2228	7	US-11-174-307B-920	Sequence 920, App
38	98	10.0	2804	6	US-10-541-708-48	Sequence 48, Appl
39	97.5	9.9	197	7	US-11-211-917-139	Sequence 139, App
40	97.5	9.9	277	6	US-10-511-937-2455	Sequence 2455, Ap
41	97.5	9.9	277	6	US-10-511-937-2518	Sequence 2518, Ap
42	97.5	9.9	277	7	US-11-170-797-5	Sequence 5, Appli
43	97	9.9	655	6	US-10-505-928-843	Sequence 843, App
44	97	9.9	655	6	US-10-196-749-418	Sequence 418, App
45	96.5	9.8	909	6	US-10-449-902-44686	Sequence 44686, A



This page gives you Search Results detail for the Application 10660968 and Search Result us-10-660-968a-38.rpr.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:51:11 ; Search time 39 Seconds  
(without alignments)  
426.808 Million cell updates/sec

Title: US-10-660-968A-38  
Perfect score: 980  
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....QRRNLSSPCHPARRPVLSPK 173

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	137.5	14.0	454	1	GQMST1	tumor necrosis fac
2	135	13.8	260	1	A46517	CD27 antigen precu
3	132	13.5	461	1	A35356	tumor necrosis fac
4	127	13.0	250	1	A49053	CD27 antigen precu
5	127	13.0	461	1	GQRTT1	tumor necrosis fac
6	126	12.9	335	2	A40036	apoptosis-mediati
7	126	12.9	461	2	JC4302	tumor necrosis fac
8	125.5	12.8	314	2	I37383	FAS soluble protei
9	125	12.8	327	2	A46484	apoptosis-mediati
10	122	12.4	435	2	I54182	tumor necrosis fac
11	122	12.4	459	2	I48854	gene murine tumour
12	122	12.4	474	2	B38634	tumor necrosis fac

13	121	12.3	255	2	I38426	lymphocyte activat
14	117.5	12.0	256	2	B32393	T-cell antigen 4-1
15	117.5	12.0	324	2	JC2395	Fas antigen precu
16	114.5	11.7	271	2	S12783	OX40 antigen precu
17	114.5	11.7	326	1	GQVZML	T2 protein - myxom
18	113	11.5	272	2	I48700	gene ox40 protein
19	113	11.5	455	1	GQHUT1	tumor necrosis fac
20	110.5	11.3	1639	1	MMFFB2	laminin gamma-1 ch
21	108	11.0	1548	2	S34583	serine proteinase
22	107.5	11.0	570	2	T37314	probable kexin (EC
23	107.5	11.0	942	2	D87803	protein bli-4D [im
24	106.5	10.9	400	1	ZBBEI4	44.1K zinc-binding
25	104	10.6	1299	2	T43251	furin (EC 3.4.21.7
26	103.5	10.6	595	2	A42086	CD30 antigen precu
27	103.5	10.6	1680	2	A43434	furin (EC 3.4.21.7
28	103.5	10.6	3635	2	T10053	laminin alpha 5 ch
29	102.5	10.5	651	2	JC7705	death receptor-6 -
30	101.5	10.4	348	2	T28623	hypothetical prote
31	101.5	10.4	349	2	D36858	gene G4R protein -
32	101.5	10.4	349	2	D72175	G2R protein - vari
33	101.5	10.4	1006	2	JC5526	kinase-defective E
34	101	10.3	3084	1	MMMSA	laminin alpha-1 ch
35	100	10.2	416	1	JN0006	nerve growth facto
36	98.5	10.1	425	1	A26431	nerve growth facto
37	98	10.0	2813	1	VWHU	von Willebrand fac
38	98	10.0	3075	2	S14458	laminin alpha-1 ch
39	97.5	9.9	277	2	A60771	B-cell activation
40	97.5	9.9	277	2	I37552	OX40 homolog - hum
41	97.5	9.9	677	2	C42125	trophozoite cystei
42	97.5	9.9	788	2	T25061	hypothetical prote
43	97.5	9.9	1713	2	A55347	adhesive ligand ep
44	97.5	9.9	1827	2	T34288	hypothetical prote
45	97	9.9	2823	2	F87908	protein T22A3.8 [i

This page gives you Search Results detail for the Application 10660968 and Search Result us-10-660-968a-38.rup.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:47:41 ; Search time 300 Seconds  
(without alignments)  
533.426 Million cell updates/sec

Title: US-10-660-968A-38  
Perfect score: 980  
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....QRRNLSSPCHPARRPVLSPK 173

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query					Description
	Score	Match Length DB	ID			
1	810	82.7	297 1	TNR27_HUMAN		Q9hav5 homo sapien
2	806	82.2	297 2	Q5VYY0_HUMAN		Q5vyy0 homo sapien
3	806	82.2	318 2	Q5VYX9_HUMAN		Q5vyx9 homo sapien
4	728	74.3	297 1	TNR27_MOUSE		Q8bx35 mus musculu
5	728	74.3	297 2	Q3KP88_MOUSE		Q3kp88 mus musculu
6	721	73.6	185 2	Q8BJS6_MOUSE		Q8bjs6 mus musculu
7	443.5	45.3	203 2	Q5VZF9_HUMAN		Q5vzf9 homo sapien
8	443.5	45.3	417 2	Q5VZF7_HUMAN		Q5vzf7 homo sapien
9	443.5	45.3	423 1	TNR19_HUMAN		Q9ns68 homo sapien
10	443.5	45.3	423 2	Q5VZF8_HUMAN		Q5vzf8 homo sapien
11	438.5	44.7	416 2	Q8BUM7_MOUSE		Q8bum7 mus musculu
12	437.5	44.6	416 1	TNR19_MOUSE		Q9jl13 mus musculu
13	437.5	44.6	416 2	Q80T13_MOUSE		Q80t13 mus musculu
14	324	33.1	168 2	Q5RBW5_PONPY		Q5rbw5 pongo pygma

15	322	32.9	120	2	Q5VZF6_HUMAN	Q5vzf6	homo sapien
16	168	17.1	448	2	Q5EFZ7_CHICK	Q5efz7	gallus gall
17	168	17.1	480	2	Q68DL5_HUMAN	Q68dl5	homo sapien
18	167	17.0	448	1	EDAR_HUMAN	Q9une0	homo sapien
19	167	17.0	448	2	Q52LL5_HUMAN	Q52ll5	homo sapien
20	158	16.1	448	1	EDAR_MOUSE	Q9r187	mus musculu
21	158	16.1	448	2	Q6NV51_MOUSE	Q6nv51	mus musculu
22	157.5	16.1	186	2	Q49PC5_9POXV	Q49pc5	vaccinia vi
23	157.5	16.1	186	2	Q49Q57_9POXV	Q49q57	vaccinia vi
24	157.5	16.1	186	2	Q911R5_9POXV	Q911r5	vaccinia vi
25	156.5	16.0	186	2	O72735_COWPX	O72735	cowpox viru
26	156.5	16.0	453	2	Q7T0R8_XENLA	Q7t0r8	xenopus lae
27	156	15.9	451	2	Q6DF68_XENTR	Q6df68	xenopus tro
28	153.5	15.7	186	2	Q9WJB4_9POXV	Q9wjb4	vaccinia vi
29	151.5	15.5	436	2	Q497Z8_MOUSE	Q497z8	mus musculu
30	150.5	15.4	186	2	Q9YP87_COWPX	Q9yp87	cowpox viru
31	148	15.1	514	1	EDAR_ORYLA	Q90vy2	oryzias lat
32	144	14.7	251	2	Q501W2_RAT	Q501w2	rattus norv
33	144	14.7	302	2	Q9PUS0_SALFO	Q9pus0	salvelinus
34	143.5	14.6	430	1	TR19L_MACFA	Q9n092	macaca fasc
35	143.5	14.6	436	1	TR19L_MOUSE	Q8bx43	mus musculu
36	143	14.6	332	1	TNR6_PIG	O77736	sus scrofa
37	142.5	14.5	415	1	TNR3_MOUSE	P50284	mus musculu
38	142.5	14.5	415	2	Q3UK82_MOUSE	Q3uk82	mus musculu
39	142	14.5	328	2	Q4RX52_TETNG	Q4rx52	tetraodon n
40	141.5	14.4	276	2	Q9DDD2_CHICK	Q9ddd2	gallus gall
41	140.5	14.3	389	2	Q6NUU6_BRARE	Q6nuu6	brachydanio
42	140.5	14.3	430	1	TR19L_HUMAN	Q969z4	homo sapien
43	139.5	14.2	283	1	TNR14_HUMAN	Q92956	homo sapien
44	139.5	14.2	283	2	Q6IB95_HUMAN	Q6ib95	homo sapien
45	137.5	14.0	350	2	O57116_COWPX	O57116	cowpox viru